

Applicant : Katia Georgopoulos et al.
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Page : 4

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REMARKS


Applicant hereby submits that the enclosures fulfill the requirements under 37 C.F.R. § 1.821-1.825. The amendments in the specification merely replace the paper copy of the Sequence Listing with an amended Sequence Listing and insert sequence identifiers in the specification. The amended Sequence Listing has been amended to include the sequences disclosed in Figures 2, 4, and 5B, and also the DNA sequence disclosed on page 47 in the description of Figure 5B. No new matter has been added.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment.

Please apply any charges or credits to Deposit Account No. 06-1050.

Respectfully submitted,

Date: 6/11/01


Laurie Butler Lawrence
Reg. No. 46,593

Fish & Richardson P.C.
225 Franklin Street
Boston, MA 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906

“Version With Markings to Show Changes Made”

In the specification:

Paragraph beginning at page 47, line 16, has been amended as follows:

Fig. 1 is a diagram depicting mouse Aiolos cDNA. 1A: is a mouse Aiolos cDNA nucleotide sequence (SEQ ID NO:1). 1B: is a corresponding amino acid sequence 507 amino acids in length (SEQ ID NO:2).

Paragraph beginning at page 47, line 19, has been amended as follows:

Fig. 2 is a diagram depicting homology at the amino acid level between the mouse (amino acid residues 275 to 507 of SEQ ID NO:2) and chicken (SEQ ID NO:30) Aiolos sequence and the mouse (amino acid residues 283 to 518 of SEQ ID NO:27) and chicken Ikaros exon 7 (SEQ ID NO:31) sequence.

Paragraph beginning at page 47, line 22, has been amended as follows:

Fig. 3 is a diagram depicting the homology between mouse Aiolos amino acid [sequence] sequence (amino acid residues 109 to 305 of SEQ ID NO:2) and mouse Ikaros amino acid [sequence] sequence (amino acid residues 1 to 310 of SEQ ID NO:27).

Paragraph beginning at page 47, line 25, has been amended as follows:

Fig. 4 is a diagram depicting Aiolos exons (exon 3: SEQ ID NO:32; exon 4: SEQ ID NO:33; exon 5: SEQ ID NO:34; exon 6: SEQ ID NO:35; exon 7: SEQ ID NO:36). Based on homology to Ikaros, the exons encoding different segments of the Aiolos gene are deduced. The exon boundaries of exons 5/6 and 6/7 have been confirmed from genomic sequence (6/7) or from differential splice products (5/6). Three classes of cDNA were recovered. The first contains exons 3 through 7. A second class splices exon 5 directly to exon 7, skipping exon 6. The third contains exon 7 and contiguous genomic sequence extending upstream of this exon.

Paragraph beginning at page 47, line 32, has been amended as follows:

Fig. 5A: is a human Aiolos cDNA nucleotide sequence. Consensus sequence of human Aiolos cDNA from RTPCR using mouse AioF primer (ex3) in forward direction and human hAio2 primer (ex6) in reverse direction. This sequence does not include the AioF primer sequence but does include the hAio2 sequence. AioF = atg aaa gtg aaa gat gaa tac agc (SEQ ID NO:38) only human sequence is shown here. EcoRI sites flank directly 5' and 3'. The cDNA sequence in figure 5A is SEQ ID NO: 7. 5B: shows a corresponding human amino acid sequence 209 amino acids in length (SEQ ID NO:8). 5B also shows the corresponding mouse sequence and shows regions of shared sequence (amino acid residues 66 to 273 of SEQ ID NO:2). The [human protein] consensus sequence in 5B is SEQ ID NO:[8]37.

Paragraph beginning at page 48, line 4, has been amended as follows:

Fig. 6 is a diagram depicting comparison of the amino acid sequence of Aiolos (top sequence; SEQ ID NO:2) and Ikaros (bottom sequence; SEQ ID NO:27) proteins. The boxed methionines represent the three translation initiation codons. The boxed cysteines and histidines represent the paired cysteines and histidines of the zinc finger motifs. The conserved activation domain (amino acids 290-344 of Aiolos protein) is shaded. Identical residues are indicated by bars and conservative residues are indicated by dots.